PCT10

RAW SEQUENCE LISTING   DATE: 03/21/2002
PATENT APPLICATION: US/10/070,464   TIME: 14:58:24

Input Set : A:\GH-007-SEQLIST.TXT
Output Set: N:\CRF3\03212002\J070464.raw

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   4 <110> APPLICANT: ABBOTT, Catherine Anne
   5          GORRELL, Mark Douglas
   7 <120> TITLE OF INVENTION: DIPEPTIDYL PEPTIDASES
  10 <130> FILE REFERENCE: GH-007
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/070,464
C--> 12 <141> CURRENT FILING DATE: 2002-03-07
  12 <150> PRIOR APPLICATION NUMBER: PCT/AU00/01085
  13 <151> PRIOR FILING DATE: 2000-09-11
  15 <150> PRIOR APPLICATION NUMBER: AU PQ5709
  16 <151> PRIOR FILING DATE: 2000-02-18
  18 <150> PRIOR APPLICATION NUMBER: AU PQ2762
  19 <151> PRIOR FILING DATE: 1999-09-10
  21 <160> NUMBER OF SEQ ID NOS: 8
  23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
  25 <210> SEQ ID NO: 1
  26 <211> LENGTH: 882
  27 <212> TYPE: PRT
  28 <213> ORGANISM: Homo Sapiens
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  33 Thr Ala Asp Cys Glu Glu Asn Ile Glu Ser Gln Asp Arg Pro Lys Leu
  34              20                  25                  30
  35 Glu Pro Phe Tyr Val Glu Arg Tyr Ser Trp Ser Gln Leu Lys Lys Leu
  36          35                  40                  45
  37 Leu Ala Asp Thr Arg Lys Tyr His Gly Tyr Met Met Ala Lys Ala Pro
  38      50                  55                  60
  39 His Asp Phe Met Phe Val Lys Arg Asn Asp Pro Asp Gly Pro His Ser
  40  65                  70                  75                  80
  41 Asp Arg Ile Tyr Tyr Leu Ala Met Ser Gly Glu Asn Arg Glu Asn Thr
  42                  85                  90                  95
  43 Leu Phe Tyr Ser Glu Ile Pro Trp Ser Ile Asn Ala Ala Ala Val Leu
  44              100                 105                 110
  45 Met Leu Ser Trp Lys Pro Leu Leu Asp Leu Phe Gln Ala Thr Leu Arg
  46          115                 120                 125
  47 Tyr Gly Met Tyr Ser Arg Glu Glu Glu Leu Leu Arg Glu Arg Lys Arg
  48      130                 135                 140
  49 Ile Gly Thr Val Gly Ile Ala Ser Tyr Asp Tyr His Gln Gly Ser Gly
  50  145                 150                 155                 160
  51 Thr Phe Leu Phe Gln Ala Gly Ser Gly Ile Tyr His Val Lys Asp Gly
  52              165                 170                 175
  53 Gly Pro Gln Gly Phe Thr Gln Gln Pro Leu Arg Pro Asn Leu Val Glu
  54              180                 185                 190
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55 Thr Ser Cys Pro Asn Ile Arg Met Asp Pro Lys Leu Cys Pro Ala Asp
56         195             200             205
57 Pro Asp Trp Ile Ala Phe Ile His Ser Asn Asp Ile Trp Ile Ser Asn
58     210             215             220
59 Ile Val Thr Arg Glu Glu Arg Arg Leu Thr Tyr Val His Asn Glu Leu
60 225             230             235             240
61 Ala Asn Met Glu Glu Asp Ala Arg Ser Ala Gly Val Ala Thr Phe Val
62         245             250             255
63 Leu Gln Glu Glu Phe Asp Arg Tyr Ser Gly Tyr Trp Trp Cys Pro Lys
64         260             265             270
65 Ala Glu Thr Thr Pro Ser Gly Gly Lys Ile Leu Arg Ile Leu Tyr Glu
66         275             280             285
67 Glu Asn Asp Glu Ser Glu Val Glu Ile Ile His Val Thr Ser Pro Met
68     290             295             300
69 Leu Glu Thr Arg Arg Ala Asp Ser Phe Arg Tyr Pro Lys Thr Gly Thr
70 305             310             315             320
71 Ala Asn Pro Lys Val Thr Phe Lys Met Ser Glu Ile Met Ile Asp Ala
72         325             330             335
73 Glu Gly Arg Ile Ile Asp Val Ile Asp Lys Glu Leu Ile Gln Pro Phe
74         340             345             350
75 Glu Ile Leu Phe Glu Gly Val Glu Tyr Ile Ala Arg Ala Gly Trp Thr
76         355             360             365
77 Pro Glu Gly Lys Tyr Ala Trp Ser Ile Leu Leu Asp Arg Ser Gln Thr
78     370             375             380
79 Arg Leu Gln Ile Val Leu Ile Ser Pro Glu Leu Phe Ile Pro Val Glu
80 385             390             395             400
81 Asp Asp Val Met Glu Arg Gln Arg Leu Ile Glu Ser Val Pro Asp Ser
82         405             410             415
83 Val Thr Pro Leu Ile Ile Tyr Glu Glu Thr Thr Asp Ile Trp Ile Asn
84         420             425             430
85 Ile His Asp Ile Phe His Val Phe Pro Gln Ser His Glu Glu Glu Ile
86         435             440             445
87 Glu Phe Ile Phe Ala Ser Glu Cys Lys Thr Gly Phe Arg His Leu Tyr
88     450             455             460
89 Lys Ile Thr Ser Ile Leu Lys Glu Ser Lys Tyr Lys Arg Ser Ser Gly
90 465             470             475             480
91 Gly Leu Pro Ala Pro Ser Asp Phe Lys Cys Pro Ile Lys Glu Glu Ile
92         485             490             495
93 Ala Ile Thr Ser Gly Glu Trp Glu Val Leu Gly Arg His Ile Ser Asn
94         500             505             510
95 Ile Glu Val Asp Glu Val Arg Arg Leu Val Tyr Phe Glu Glu Thr Lys
96     515             520             525
97 Asp Ser Pro Leu Glu His His Leu Tyr Val Val Ser Tyr Val Asn Pro
98     530             535             540
99 Gly Glu Val Thr Arg Leu Thr Asp Arg Gly Tyr Ser His Ser Cys Cys
100 545             550             555             560
101 Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys Tyr Ser Asn Gln Lys
102         565             570             575
103 Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser Ser Pro Glu Asp Asp
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Input Set : A:\GH-007-SEQLIST.TXT
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104          580                585                590
105 Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr Ile Leu Asp Ser Ala
106          595                600                605
107 Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile Phe Ser Phe Glu Ser
108      610                615                620
109 Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr Lys Pro His Asp Leu
110 625                630                635                640
111 Gln Pro Gly Lys Lys Tyr Pro Thr Val Leu Phe Ile Tyr Gly Gly Pro
112              645                650                655
113 Gln Val Gln Leu Val Asn Asn Arg Phe Lys Gly Val Lys Tyr Phe Arg
114          660                665                670
115 Leu Asn Thr Leu Ala Ser Leu Gly Tyr Val Val Val Val Ile Asp Asn
116          675                680                685
117 Arg Gly Ser Cys His Arg Gly Leu Lys Phe Glu Gly Ala Phe Lys Tyr
118      690                695                700
119 Lys Met Gly Gln Ile Glu Ile Asp Asp Gln Val Glu Gly Leu Gln Tyr
120 705                710                715                720
121 Leu Ala Ser Arg Tyr Asp Phe Ile Asp Leu Asp Arg Val Gly Ile His
122              725                730                735
123 Gly Trp Ser Tyr Gly Gly Tyr Leu Ser Leu Met Ala Leu Met Gln Arg
124              740                745                750
125 Ser Asp Ile Phe Arg Val Ala Ile Ala Gly Ala Pro Val Thr Leu Trp
126          755                760                765
127 Ile Phe Tyr Asp Thr Gly Tyr Thr Glu Arg Tyr Met Gly His Pro Asp
128      770                775                780
129 Gln Asn Glu Gln Gly Tyr Tyr Leu Gly Ser Val Ala Met Gln Ala Glu
130 785                790                795                800
131 Lys Phe Pro Ser Glu Pro Asn Arg Leu Leu Leu Leu His Gly Phe Leu
132              805                810                815
133 Asp Glu Asn Val His Phe Ala His Thr Ser Ile Leu Leu Ser Phe Leu
134          820                825                830
135 Val Arg Ala Gly Lys Pro Tyr Asp Leu Gln Ile Tyr Pro Gln Glu Arg
136          835                840                845
137 His Ser Ile Arg Val Pro Glu Ser Gly Glu His Tyr Glu Leu His Leu
138      850                855                860
139 Leu His Tyr Leu Gln Glu Asn Leu Gly Ser Arg Ile Ala Ala Leu Lys
140 865                870                875                880
141 Val Ile
```

146 <211> LENGTH: 3120
148 <213> ORGANISM: Homo Sapiens

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152 cgttcgccgc ctgggttatc accgacacca ccgccgagga agccactgca accaggaccg 120
153 gagtgaggc ggcgcagcat gaagcggcgc aggccgcctc catagcgcac gtcggacgg 180
154 tccgggcggg gcgggggga aggaaaatgc gacatggcag cagcaatgga aacagaacag 240
155 ctgggtgttg agatatttga aactgcggac tgtgaggaga atattgaatc acaggatcgg 300
156 cctaaattgg agccttttta tgttgagcgg tattcctgga gtcagcttaa aaagctgctt 360
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157 gccgatacca gaaaatatca tggctacatg atggctaagg caccacatga tttcatgttt 420
158 gtgaagagga atgatccaga tggacctcat tcagacagaa tctattacct tgccatgtct 480
159 ggtgagaaca gagaaaatac actgttttat tctgaaattc ccaaaactat caatagagca 540
160 gcagtcttaa tgctctcttg gaagcctctt ttggatcttt ttcagcaac actggactat 600
161 ggaatgtatt ctcgagaaga agaactatta agagaaagaa aacgcattgg aacagtcgga 660
162 attgcttctt acgattatca ccaaggaagt ggaacatttc tgtttcaagc cggtagtgga 720
163 atttatcacg taaaagatgg agggccacaa ggatttacgc aacaaccttt aaggcccaat 780
164 ctagtggaaa ctagttgtcc caacatacgg atggatccaa aattatgccc cgctgatcca 840
165 gactggattg ctttttataca tagcaacgat atttggatat ctaacatcgt aaccagagaa 900
166 gaaaggagac tcacttatgt gcacaatgag ctagccaaca tggaagaaga tgccagatca 960
167 gctggagtcg ctacctttgt tctccaagaa gaatttgata gatattctgg ctattggtgg 1020
168 tgtccaaaag ctgaaacaac tcccagtggt ggtaaaattc ttagaattct atatgaagaa 1080
169 aatgatgaat ctgaggtgga aattattcat gttacatccc ctatgttgga aacaaggagg 1140
170 gcagattcat tccgttatcc taaaacaggt acagcaaatc ctaaagtcac ttttaagatg 1200
171 tcagaaataa tgattgatgc tgaaggaagg atcatagatg tcatagataa ggaactaatt 1260
172 caacctttg agattctatt tgaaggagtt gaatatattg ccagagctgg atggactcct 1320
173 gagggaaaat atgcttggtc catcctacta gatcgctccc agactcgcct acagatagtg 1380
174 ttgatctcac ctgaattatt tatcccagta gaagatgatg ttatggaaag gcagagactc 1440
175 attgagtcag tgcctgattc tgtgacgcca ctaattatct atgaagaaac aacagacatc 1500
176 tggataaaata tccatgacat ctttcatgtt tttcccaaa gtcacgaaga ggaaattgag 1560
177 tttatttttg cctctgaatg caaaacagt ttccttcatt tatacaaaat tacatctatt 1620
178 ttaaaggaaa gcaaatataa acgatccagt ggtgggctgc ctgctccaag tgatttcaag 1680
179 tgtcctatca aagaggagat agcaattacc agtggtgaat gggaagttct tggccggcat 1740
180 ggatctaata tccaagttga tgaagtcaga aggctggtat attttgaagg caccaaagac 1800
181 tcccctttag agcatcacct gtacgtagtc agttacgtaa atcctggaga ggtgacaagg 1860
182 ctgactgacc gtggctactc acattcttgc tgcatcagtc agcactgtga cttctttata 1920
183 agtaagtata gtaaccagaa gaatccacac tgtgtgtccc tttacaagct atcaagtcct 1980
184 gaagatgacc caacttgcaa aacaaaggaa ttttgggcca ccatttggga ttcagcaggt 2040
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190 gaaattgacg atcaggtgga aggactccaa tatctagctt ctcgatatga tttcattgac 2400
191 ttagatcgtg tgggcatcca cggctggtcc tatggaggat acctctcct gatggcatta 2460
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193 ttctatgata caggatacac ggaacgttat atgggtcacc ctgaccagaa tgaacagggc 2580
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195 aagacttttt ag ataa aataat  aca aa aaaa 2700
196 agttttttag tgaggctgg aaagccatat gatttacaga tctatcctca ggagagacac 2760
197 aacataagag ttcctgaatc gggagaacat tatgaactgc atgtttgca ctacttcaa 2820
198 gaagacctg gatcacgtat tgctgctcta aaagtgatat aattttgacc tgtgtggacc 2880
199 tctctggtat acactggcta tttaaccaaa tgaggaggtt taatcaacag aaaacacaga 2940
200 attgatcatc acatttgat acctgccatg taacatctac tcctgaaaat aaatgtggtg 3000
201 ccatgcaggg gtctacgttt tgtggtagta atctaatacc ttaaccccac atgctcaaaa 3060
202 tcaaatgata catattcctg agagacccag caataccata agaattacta aaaaaaaaaa 3120
205 <210> SEQ ID NO: 3
206 <211> LENGTH: 310
207 <212> TYPE: PRT
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RAW SEQUENCE LISTING   DATE: 03/21/2002
PATENT APPLICATION: US/10/070,464   TIME: 14:58:24

Input Set : A:\GH-007-SEQLIST.TXT
Output Set: N:\CRF3\03212002\J070464.raw

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208 <213> ORGANISM: Homo Sapiens
210 <400> SEQUENCE: 3
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214              20                  25                  30
215 Ser His Ser Cys Cys Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys
216          35                  40                  45
217 Tyr Ser Asn Gln Lys Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser
218      50                  55                  60
219 Ser Pro Glu Asp Asp Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr
220 65                  70                  75                  80
221 Ile Leu Asp Ser Ala Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile
222              85                  90                  95
223 Phe Ser Phe Glu Ser Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr
224             100                 105                 110
225 Lys Pro His Asp Leu Gln Pro Gly Lys Lys Tyr Pro Thr Val Leu Phe
226         115                 120                 125
227 Ile Tyr Gly Gly Pro Gln Gly Gln Ile Glu Ile Asp Asp Gln Val Glu
228     130                 135                 140
229 Gly Leu Gln Tyr Leu Ala Ser Arg Tyr Asp Phe Ile Asp Leu Asp Arg
230 145                 150                 155                 160
231 Val Gly Ile His Gly Trp Ser Tyr Gly Gly Tyr Leu Ser Leu Met Ala
232             165                 170                 175
233 Leu Met Gln Arg Ser Asp Ile Phe Arg Val Ala Ile Ala Gly Ala Pro
234             180                 185                 190
235 Val Thr Leu Trp Ile Phe Tyr Asp Thr Gly Tyr Thr Glu Arg Tyr Met
236         195                 200                 205
237 Gly His Pro Asp Gln Asn Glu Gln Gly Tyr Tyr Leu Gly Ser Val Ala
238     210                 215                 220
239 Met Gln Ala Glu Lys Phe Pro Ser Glu Pro Asn Arg Leu Leu Leu Leu
240 225                 230                 235                 240
241 His Gly Phe Leu Asp Glu Asn Val His Phe Ala His Thr Ser Ile Leu
242             245                 250                 255
243 Leu Ser Phe Leu Val Arg Ala Gly Lys Pro Tyr Asp Leu Gln Ile Tyr
244             260                 265                 270
245 Pro Gln Glu Arg His Ser Ile Arg Val Pro Glu Ser Gly Glu His Tyr
246         275                 280                 285
247 . . . . . . . Ala Leu . . . . . . Tyr . . . . Il . . Asn Leu Gly  Ser Arg Ile
248         290                 295                 300
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250 305                 310
253 <210> SEQ ID NO: 4
254 <211> LENGTH: 1197
255 <212> TYPE: DNA
256 <213> ORGANISM: Homo Sapiens
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260 atcctggaga ggtgacaagg ctgactgacc gtggctactc acattcttgc tgcatcagtc 120
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VERIFICATION SUMMARY   DATE: 03/21/2002
PATENT APPLICATION: **US/10/070,464**   TIME: 14:58:25

Input Set : **A:\GH-007-SEQLIST.TXT**
Output Set: **N:\CRF3\03212002\J070464.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date